A Conjecture of Reconstructing GTPase Pathway Networks (Algebra, Languages and Computation)

AUTHOR(S):

Liu, Jian-Qin; Shimohara, Katsunori

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Jian-Qin Liu and Katsunori Shimohara

ATR Network Informatics Laboratories,

2-2-2 Hikaridai, "Keihanna Science City", Kyoto 619-0288, Japan

e-mail: {jqliu, katsu}@atr.jp

Abstract: In bioinformatics, two kinds of pathways – metabolic pathways and signaling pathways – are important. The former directly determines the sustaining of the cellular system and the latter acts as the main mechanism for signal transduction and cell communication. From biochemical experiments, simple pathways can be recognized. But, complex networks formed by the interactions of the known simple pathways can not be recognized easily owing to the existence of crosstalk among these known pathways. In order to systematically understand the behavior of GTPase pathways that belong to the second kind of pathways in cells, we have to study the structure of GTPase pathway network under the condition of unknown crosstalks. We propose a conjecture of reconstructing GTPase pathway networks from atomic pathways of GTPase switches. These atomic pathways refer to those GTPase pathways that determine the binary values of GTPases and can not be divided further.

Let PN-set = $\{PN_0, PN_1, \ldots, PN_{L-1}\}$, where PN_i ($i = 0, 1, \ldots, L-1, L \in N$) refers to the atomic pathway of GTPase switch. Assuming that the cross-talks among these pathways exist, we have that

CONJECTURE:

If we can find an algorithm ϑ for reconstructing GTPase pathway networks, the time complexity of the reconstruction process by ϑ is NP under the condition that there is no known knowledge about the interactions of the GTPase switches.

Keywords: NP problems, algorithmic design, bioinformatics.

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